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Cofilin/Actin Interactions

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ABSTRACT: Synchrotron footprinting has been successfully used to visualize the detailed tertiary structure changes during RNA folding and in DNA-Protein binding. Recently we have further developed this technique to analyzing protein structure. In this project we use synchrotron protein footprinting to analyze protein/protein interactions by mapping the binding surface of cofilin in the cofilin/G-actin complex. Biochemical and genetic data have suggested an "actin binding face" for cofilin that covers the N-terminal segments α1 and β1, and α3 helix. Our footprinting results confirm this binding face. However, we found that Leu21 at the end of α1 does not contribute to the binding site while Pro94 at the end of α3 does. Our footprinting results also showed that Leu108 and Leu112 are potential binding sites and that Phe124 in the loop between β6 and α4 is not protected upon G-actin binding.